#3

OIPE

RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/050,200   TIME: 19:10:29

Input Set : **A:\ort-1417seqlst.txt**
Output Set: **N:\CRF3\02062002\J050200.raw**

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 3 <110> APPLICANT: Fourie, Anne
 4         Coles, Fawn
 5         Karlsson, Lars
 7 <120> TITLE OF INVENTION: Aggrecanase-1 and -2 Peptide Substrates and Methods
 9 <130> FILE REFERENCE: ORT-1417
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C--> 11 **<140> CURRENT APPLICATION NUMBER: US/10/050,200**
C--> 11 **<141> CURRENT FILING DATE: 2002-01-16**

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   11 <160> NUMBER OF SEQ ID NOS: 60
   13 <170> SOFTWARE: PatentIn version 3.1
   15 <210> SEQ ID NO: 1
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   17 <212> TYPE: DNA
   18 <213> ORGANISM: Homo sapiens
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   21 <221> NAME/KEY: misc_feature
   22 <222> LOCATION: (1)..(1359)
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   31 cttctgctac tgctggcctc tctcctgccc tcagcccggc tggccagccc cctcccccgg     180
   33 gaggaggaga tcgtgtttcc agagaagctc aacggcagcg tcctgcctgg ctcgggcacc     240
   35 cctgccaggc tgttgtgccg cttgcaggcc tttggggaga cgctgctact agagctggag     300
   37 caggactccg gtgtgcaggt cgaggggctg acagtgcagt acctgggcca ggcgcctgag     360
   39 ctgctgggtg gagcagagcc tggcacctac ctgactggca ccatcaatgg agatccggag     420
   41 tcggtggcat ctctgcactg ggatggggga ccctgttag gcgtgttaca atatcggggg     480
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   65 atcagtttga atgggccttt gagcacctct cgccatgtca tggcccctgt gatggctcat    1200
   67 gtggatcctg aggagccctg gtccccctgc agtgcccgct tcatcactga cttcctggac    1260
   69 aatggctatg gcactgtct cttagacaaa ccagaggctc cattgcatct gcctgtgact    1320
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 77 <213> ORGANISM: Homo sapiens
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 80 <221> NAME/KEY: misc_feature
 81 <222> LOCATION: (1)..(1516)
 82 <223> OTHER INFORMATION: truncated Aggrecanse-2
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 90 gactgctgca gcagccgccc agccccgccg gcggcagggg gaggaggtgc aggagcgagc    180
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120 caccacactc aagaactttt gcaagtggca gcaccaacac aaccagctgg gagatgacca   1080
122 tgaggagcac tacgatgcag ctatcctgtt tactcgggag gatttatgtg ggcatcattc   1140
124 atgtgacacc ctgggaatgg cagacgttgg gaccatatgt tctccagagc gcagctgtgc   1200
126 tgtgattgaa gacgatggcc tccacgcagc cttcactgtg gctcacgaaa tcggacattt   1260
128 acttggcctc tcccatgacg attccaaatt ctgtgaagag acctttggtt ccacagaaga   1320
130 taagcgctta atgtcttcca tccttaccag cattgatgca tctaagccct ggtccaaatg   1380
132 cacttcagcc accatcacag aattcctgga tgatggccat ggtaactgtt tgctggacct   1440
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140 <211> LENGTH: 11
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: peptide substrate
147 <400> SEQUENCE: 3
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150 1               5                   10
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154 <211> LENGTH: 11
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Peptide substrate
161 <400> SEQUENCE: 4
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168 <211> LENGTH: 10
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Peptide substrate
175 <400> SEQUENCE: 5
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178 1   5   10
181 <210> SEQ ID NO: 6
182 <211> LENGTH: 10
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Peptide Substrate
189 <400> SEQUENCE: 6
191 Glu Lys Ala Arg Val Leu Ala Glu Ala Met
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196 <211> LENGTH: 13
197 <212> TYPE: PRT
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Peptide substrate
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209 <210> SEQ ID NO: 8
210 <211> LENGTH: 447
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212 <213> ORGANISM: Homo sapiens
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215 <221> NAME/KEY: MISC_FEATURE
216 <222> LOCATION: (1)..(447)
217 <223> OTHER INFORMATION: truncated Aggrecanase 1
220 <400> SEQUENCE: 8
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227   20   25   30
230 Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser
231   35   40   45
234 Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro
235   50   55   60
238 Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Thr Pro Ala Arg
239 65   70   75   80
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246 Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu
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250 Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu
251         115             120             125
254 Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp
255      130             135             140
258 Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu
259 145             150             155             160
262 His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro
263             165             170             175
266 Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro
267         180             185             190
270 Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg
271         195             200             205
274 Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val
275      210             215             220
278 Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
279 225             230             235             240
282 Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro
283             245             250             255
286 Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu
287         260             265             270
290 Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr
291         275             280             285
294 Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp
295      290             295             300
298 Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
299 305             310             315             320
302 Leu Cys Gly Val Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
303             325             330             335
306 Thr Val Cys Asp Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly
307         340             345             350
310 Leu Gln Ser Ala Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn
311         355             360             365
314 Met Leu His Asp Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu
315      370             375             380
318 Ser Thr Ser Arg His Val Met Ala Pro Val Met Ala His Val Asp Pro
319 385             390             395             400
322 Glu Glu Pro Trp Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu
323             405             410             415
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334 <210> SEQ ID NO: 9
335 <211> LENGTH: 492
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
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Input Set : A:\ort-1417seqlst.txt
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340 <221> NAME/KEY: MISC_FEATURE
341 <222> LOCATION: (1)..(492)
342 <223> OTHER INFORMATION: truncated Aggrecanse-2
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352             20                  25                  30
355 Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly
356             35                  40                  45
359 Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu
360     50                  55                  60
363 Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu
364 65                  70                  75                  80
367 Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg
368                 85                  90                  95
371 Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly
372             100                 105                 110
375 Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser
376             115                 120                 125
379 His Cys Phe Tyr Arg Gly Thr Val Asp Gly Ser Pro Arg Ser Leu Ala
380     130                 135                 140
383 Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His
384 145                 150                 155                 160
387 Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu
388             165                 170                 175
391 Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val
392             180                 185                 190
395 Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser
396             195                 200                 205
399 Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala
400     210                 215                 220
403 His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp
404 225                 230                 235                 240
407 Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp
408             245                 250                 255
411 Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu
412             260                 265                 270
415 Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln
416             275                 280                 285
419 His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His
420     290                 295                 300
423 Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val
424 305                 310                 315                 320
427 Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr
428             325                 330                 335
431 Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly
432             340                 345                 350
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VERIFICATION SUMMARY

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Input Set : **A:\ort-1417seqlst.txt**
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37